TCGACCCACGCGTCCGGGAGGATCGGGAGTCGCGGGAGGATGGGCCGCCGCTAGGCTCGCACTCCGGA
CGCGCCTCGC
AGTGCGCAGGGTGGGTGCCCCGCGCCTGCAGCGTCCGCCGGGGCGGCGCGGCGGGAGGTGGCCGACAG
GCTCCGGGCC
TCGCAGCCTCAGCCCCCGGCCCAGCGCGCTTTCCGACGGCGGCGCCGCGCCGAGCCACCCGCC
CGCCCAAGGTCTCTCGCGGGCGGGAGAACGGAAAACTCCCAACTTCCTGAGTTCTAAAGTTCCTGTTG
CTTCAGACAA
TGGATGAGCAATCACAAGGAATGCAAGGGCCACCTGTTCCTCAGTTCCAACCACAGAAGGCCTTACGA
CCGGATATGG
GCTATAATACATTAGCCAACTTTCGAATAGAAAAGAAAATTGGTCGCGGACAATTTAGTGAAG
TTTATAGAGCAGCCTGTCTCTTGGATGGAGTACCAGTAGCTTTAAAAAAGTGCAGATATTTGATTTA
ATGGATGCCA
AAGCACGTGCTGATTGCATCAAAGAAATAGATCTTCTTAAGCAACTCAACCATCCAAATGTAATAAAA
TATTATGCAT
CATTCATTGAAGATAATGAACTAAACATAGTTTTGGAACTAGCAGATGCTGGCGACCTATCCA
GAATGATCAAGCATTTTAAGAAGCAAAAGAGGCTAATTCCTGAAAGAACTGTTTGGAAGTATTTTGTT
CAGCTTTGCA
GTGCATTGGAACACATGCATTCTCGAAGAGTCATGCATAGAGATATAAAACCAGCTAATGTGTTCATT
ACAGCCACTG
GGGTGGTAAAACTTGGAGATCTTGGGCTTGGCCGGTTTTTTCAGCTCAAAAACCACAGCTGCAC
ATTCTTTAGTTGGTACGCCTTATTACATGTCTCCAGAGAGAATACATGAAAATGGATACAACTTCAAA
TCTGACATCT
GGTCTCTTGGCTGTCTACTATATGAGATGGCTGCATTACAAAGTCCTTTCTATGGTGACAAAATGAAT
TTATACTCAC
TGTGTAAGAAGATAGAACAGTGTGACTACCCACCTCTTCCTTCAGATCACTATTCAGAAGAAC
TCCGACAGTTAGTTAATATGTGCATCAACCCAGATCCAGAGAAGCGACCAGACGTCACCTATGTTTAT
GACGTAGCAA
AGAGGATGCATGCATGCACTGCAAGCAGCTAAACATGCAAGATCATGAAGAGTGTAACCAAAGTAATT
GAAAGTATTT
TGTGCAAAGTCGTACCTSCCCATTTATGTCTGGGTGTTAAGATTAATATTTCAGAGCTAGTGT
GCTCTGAATCCTTAACCAGTTTTCATATAAGCTTCATTTTGTACCAGTCACCTAAATCACCTCCTTGC
AACCCCCAAA
TGACTTTGGAATAACTGAATTGCATGTTAGGAGAGAAAATGAAACATGATGGTTTTGAATGGCTAAAG
GTTTATAGAA
TTTCTTACAGTTTTCTGCTGATAAATTGTGTTTAGATAGACTGTCAGTGCCAAATATTGAAGG
TGCAGCTTGGCACACATCAGAATAGACTCATACCTGAGAAAAGTATCTGAACATGTGACTTGTTTCT
TTTTTAGTAA
TTTATGGACATTGAGATGAACACAATTGTGAACTTTTGTGAAGATTTTATTTTTAAACGTTTGAAGTA
CTAGTTTTAG
TTCTTAGCAGAGTAGTTTTCAAATATGATTCTTATGATAAATGTAGACACAAACTATTTGAGA
AACATTTAGAACTCTTAGCTTATACATTCAAAATGTAACTATTAAATGTGAAGATTTGGGGACAAAAT
GTGAGTCAGA
CACTGAAGAGTTTTTTGTTTTGTTTTAATATTTTTGATATTCTCTTTGCATTGAAATGGTATAAATGA
ATCCATTTAA
AAAGTGGTTAAGGATTTGTTTAGCTGGTGTGATAATAATTTTTAAAGTTGCACATTGCCCAAG
GCTTTTTTTGTGTGTTTTTATTGTTGTTTGTACATTTGAAAAATATTCTTTGAATAACCTTGCAGTAC
TATATTTCAA

FIGURE 1

TTTCTTTATAAATTTAAGTGCATTTTAACTCATAATTGTACACTATAATATAAGCCTAAGTTTTTATT
CATAAGTTTT
ATTGAAGTTCTGATCGGTCCCCTTCAGAAATTTTTTTATATTATTCTTCAAGTTACTTTCTTA
TTTATATTGTATGTGCATTTTATCCATTAATGTTTCATACTTTCTGAGAGTATAATACCCTTTTAAAA
GATATTTGGT
ATACCAATACTTTTCCTGGATTGAAAACTTTTTTTAAACTTTTTAAAATTTGGGCCACTCTGTATGCA
TATGTTTGGT
CTTGTTAAAGAGGAAGAAAGGATGTGTGTTATACTGTACCTGTGAATGTTGATACAGTTACAA
TTTATTTGACAAGGTTGTAATTCTAGAATATGCTTAATAAAATGAAAACTGGCCATGACTACAGCCAG
AACTGTTATG
AGATTAACATTTCTATTGAGAAGCTTTTGAGTAAAGTACTGTATTTGTTCATGAAGATGACTGAGATG
GTAACACTTC
GTGTAGCTTAAGGAAATGGGCAGAATTTCGTAAATGCTGTTGTGCAGATGTGTTTTCCCTGAA
TGCTTTCGTATTAGTGGCGACCAGTTTCTCACAGAATTGTGAAGCCTGAAGGCCAAGAGGAAGTCACT
GTTAAAGGAC
TCTGTGCCATCTTACAACCTTGGATGAATTATCCTGCCAACGTGAAAACCTCATGTTCAAAGAACACT
TCCCTTTAGC
CGATGTAACTGCTGGTTTTGTTTTTCATATGTGTTTTTCTTACACTCATTTGAATGCTTTCAA
GCATTTGTAAACTTAAAAAAAANWAWAAAGGGCAAAAAGTCTGAACCCTTGTTTTCTGAAATCTAATC
AGTTATGTAT
GGTTTCTGAAGGGTAATTTTATTTTGGAATAGGTAAAGCGAAACCTGTTTTGTCWTGTTTTTCCTGAG
GGCTAGATGC
ATTTTTTTTCTCACACTCTTAATGACTTTTAACATTTATACTGAGCATCCATAGATATATTCC
TAGAAGTATGAGAAGAATTATTCTTATTGACCATTAATGTCATGTTCATTTTAATGTAATATAATTGA
GATGAAATGT
TCTCTGGTTGGAACAGATACTCTCTTTTTTTTTCTTGCAATCTTTAAGAATACATAGATCTAAAATTC
ATTAGCTTGA
CCCCTCAAAGTAACTTTTAAGTAAAGATTAAAGCTTTTCTTCTCAGTGAATATATCTGCTAGA
AGGAAATAGCTGGGAAGAATTTAATGATCAGGGAAATTCATTATTTCTATATGTGGAAACTTTTTGCT
TCGAATATTG
TATCTTTTTAAATCTAAATGTTCATATTTTTCCTGAAGAAACCACTGTGTAAAAATCAAATTTTAATT
TTGAATGGAA
TAATTTCAAAGAACTATGAAGATGATTTGAAGCTCTAATTTATATAGTCACCTATAAAATGTT
CTTTATATGTGTTCATAAGTAAATTTTATATTGATTAAGTTAAACTTTTGAATTGATTTGAGGAGCAG
TAAAATGAAA
GCTATATCTATTNCTAAACCYTATTTAGACATTGGKACCAGTTACCCAGGTGAAAATAKGGAGTAACT
TTGTTTTGTA
TGGTAAGGTTTAGGAATGGNGGATGAAGGGTATCTCTATATAAATAAAGTGCTCAACAATGTG
CAATGATTGTAAATTTAGTAAGATATTACAGCCATTTCATGAATGCTTTACCATTCAACATAGTATCT
ATTACAAAAC
ACCTTTCTTGTATCCATATACTTCAGGTGTTGCTGTTAACATTTACTATGATATTTATTTTAACCAAA
ATGTTACTCA
CATTAAATGTTTATTCTTTAAAATGAATGTATTATGTTTTTAACCCACAAATGCATACTTACC
CTGTGCCTCATATTTCAATAGTACTGTAATATGGACATCTTTTGTGAAATACTTTTATTTTGTTATGC
TTTAAATATA
CATACAAAAAGATTTCTGTTATTAGCTTTGAAAATTGTATAATATCCTAATATAAACAAAAATATAAA
AATAAAAATG
AATACAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGG

FIGURE 1 (cont'd)

MDEQSQGMQGPPVPQFQPQKALRPDMGYNTLANFRIEKKIGRGQFSEVYRAACLLDGVPVALKKVQIF
DLMDAKARAD
CIKEIDLLKQLNHPNVIKYYASFIEDNELNIVLELADAGDLSRMIKHFKKQKRLIPERTVWKYFVQLC
SALEHMHSRR
VMHRDIKPANVFITATGVVKLGDLGLGRFFSSKTTAAHSLVGTPYYMSPERIHENGYNFKSDI
WSLGCLLYEMAALQSPFYGDKMNLYSLCKKIEQCDYPPLPSDHYSEELRQLVNMCINPDPEKRPDVTY
VYDVAKRMHA
CTASS

FIGURE 1 (cont'd)

GTCGACCCACGCGTCCGGTGGAAGT●AATACTTTGTCATTATGAGATGTCGT●TCGG
TGCCTCCTTTGTGCAAATTAAATTTGATGACTTGCAGTTTTTTGAAAACTGCGGTGGAGG
AAGTTTTGGGAGTGTTTATCGAGCCAAATGGATATCACAGGACAAGGAGGTGGCTGTAAA
GAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGTGTCCTCAGTCACAGAAACAT
CATCCAGTTTTATGGAGTAATTCTTGAACCTCCCAACTATGGCATTGTCACAGAATATGC
TTCTCTGGGATCACTCTATGATTACATTAACAGTAACAGAAGTGAGGAGATGGATATGGA
TCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTATTTACATATGGAGGC
TCCTGTCAAGGTGATTCACAGAGACCTCAAGTCAAGAAACGTTGTTATAGCTGCTGATGG
AGTACTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCCATAA·C·ATACAACACACATGTC
CTTGGTTGGAACTTTCCCATGGATGGCTCCAGAAGTTATCCAGAGTCTCCCTGTGTCAGA
AACTTGTGACACATATTCCTATGGTGTGGTTCTCTGGGAGATGCTAACAAGGGAGGTCCC
CTTTAAAGGTTTGGAAGGATTACAAGTAGCTTGGCTTGTAGTGGAAAAAAACGAGAGATT
AACCATTCCAAGCAGTTGCCCCAGAAGTTTTGCTGAACTGTTACATCAGTGTTGGGAAGC
TGATGCCAAGAAACGGCCATCATTCAAGCAAATCATTTCAATCCTGGAGTCCATGTCAAA
TGACACGAGCCTTCCTGACAAGTGTAACTCATTCCTACACAACAAGGCGGAGTGGAGGTG
CGAAATTGAGGCAACTCTTGAGAGGCTAAAGAAACTAGAGCGTGATCTCAGCTTTAAGGA
GCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAAAAGCTGACAGAGCA
GTCCAACACCCCGCTTCTCTTGCCTCTTGCTGCAAGAATGTCTGAGGAGTCTTACTTTGA
ATCTAAAACAGAGGAGTCAAACAGTGCAGAGATGTCATGTCAGATCACAGCAACAAGTAA
CGGGGAGGGCCATGGCATGAACCCAAGTCTGCAGGCCATGATGCTGATGGGCTTTGGGGA
TATCTTCTCAATGAACAAAGCAGGAGCTGTGATGCATTCTGGGATGCAGATAAACATGCA
AGCCAAGCAGAATTCTTCCAAAACCACATCTAAGAGAAGGGGGAAGAAAGTCAACATGGC
TCTGGGGTTCAGTGATTTTGACTTGTCAGAAGGTGACGATGATGATGATGATGACGGTGA
GGAGGAGGATAATGACATGGATAATAGTGAATGAAAGCAGAAAGCAAAGTAATAAAATCA
CAAATGTTTGGAAAACACAAAAGTAACTTGTTTATCTCAGTCTGTACAAAAACAGTAAGG
AGGCAGAAAGCCAAGCACTGCATTTTTAGGCCAATCACATTTACATGACCGTAATTTCTT
ATCAATTCTACTTTTATTTTTGCTTACAGAAAAACGGGGGGAGAATTAAGCCAAAGAAGT
ATATTTATGAATCAGCAAATGTGGTGCCTGATTATAGAAATTTGTGATCCTATATACAAT
ATAGGACTTTTAAAGTTGTGACATTCTGGCTTTTTCTTTTAATGAATACTTTTTAGTTTG
TATTTGACTTTATTTCCTTTATTCAAATCATTTTTAAAAACTTACATTTTGAACAAACAC
TCTTAACTCCTAATTGTTCTTTGACACGTAGTAATTCTGTGACATACTTTTTTTTTCTTA
TAGCAATACACTGTAATATCAGAAATGGTTGGCCTGAGCAACCTAGTAAGACCTCGTCTC
TACTAATAATTAAAAAACTAGCTGGCATGGTAGCACACACCTGTAGTCCCAGATACTTGG
GAGGCCAAGGCAGGAGGATTGCTTGAGACCTAGCAATCAGTCAGGGCTGCAGTGAGCCAT
GATGGCACCACTGCACTCTAGCCTGGGCAAGAGAACAAGATCCTGTCTCAAAAAACAAAA
AAAAAAAAAAGGGCGGCCG

MSSLGASFVQIKFDDLQFFENCGGGSFGSVYRAKMISQDKEVAVK
KLLKIEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDMD
HIMTWATDVAKGMHYLHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFHNHTTHMS
LVGTFPWMAPEVIQSLPVSETCDTYSYGVVLWEMLTREVPFKGLEGLQVAMLVVEKNERL
TIPSSCPRSFAELLHQCWEADAKKRPSFKQIISILESMSNDTSLPDKCNSFLHNKAEWRC
EIEATLERLKKLERDLSFKEQELKERERRLKMWEQKLTEQSNTPLLLPLAARMSEESYFE
SKTEESNSAEMSCQITATSNGEGHGMNPSLQAMMLMGPGDIFSMNKAGAVMHSGMQINMQ
AKQNSSKTTSKRRGKKVNMALGFSDFDLSEGDDDDDDDGEEEDNDMDNSE

FIGURE 2

CGGTGGTGGCGGCAGCGGCGGCTGCGGGGGCACCGGGCCGCGGCGCCACCATGGCCGTGC
GACAGGCGCTGGGCCGCGGCCTGCAGCTGGGTCGAGCGCTGCTGCTGCGCTTCACGGGCA
AGCCCGGCCGGGCCTACGGCTTGGGGCGGCCGGGCCCGGCGGCGGGCTGTGTCCGCGGGG
AGCGTCCAGGCTGGGCCGCAGGACCGGGCGCGGAGCCTCGCAGGGTCGGGCTCGGGCTTC
CTAACCGTOTCCGCTTCTTCCGCCAGTCGGTGGCCGGGCTGGCGGCGCGGTTGCAGCGGC
AGTTCGTGGTGCGGGCCTGGGGCTGCGCGGGCCCTTGCGGCCGGGCAGTCTTTCTGGCCT
TCGGGCTAGGGCTGGGCCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGG
CCTGTCAGGAGATCCAGGCAATTTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTTGG
ACACGAGACGCTTGCAGGGCTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTA
AGGGCTGCAGTGCTGCTGTGTATGAAGCCACCATGCCTACATTGCCCCAGAACCTGGAGG
TGACAAAGAGCACCGGGTTGCTTCCAGGGAGAGGCCCAGGTACCAGTGCACCAGGAGAAG
GGCAGGAGCGAGCTCCGGGGGCCCCTGCCTTCCCCTTGGCCATCAAGATGATGTGGAACA
TCTCGGCAGGTTCCTCCAGCGAAGCCATCTTGAACACAATGAGCCAGGAGCTGGTCCCAG
CGAGCCGAGTGGCCTTGGCTGGGGAGTATGGAGCAGTCACTTACAGAAAATCCAAGAGAG
GTCCCAAGCAACTAGCCCCTCACCCCAACATCATCCGGGTTCTCCGCGCCTTCACCTCTT
CCGTGCCGCTGCTGCCAGGGGCCCTGGTCGACTACCCTGATGTGCTGCCCTCACGCCTCC
ACCCTGAAGGCCTGGGCCATGGCCGGACGCTGTTCCTCGTTATGAAGAACTATCCCTGTA
CCCTGCGCCAGTACCTTTGTGTGAACACACCCAGCCCCCGCCTCGCCGCCATGATGCTGC
TGCAGCTGCTGGAAGGCGTGGACCATCTGGTTCAACAGGGCATCGCGCACAGAGACCTGA
AATCCGACAACATCCTTGTGGAGCTGGACCCAGACGGCTGCCCCTGGCTGGTGATCGCAG
ATTTTGGCTGCTGCCTGGCTGATGAGAGCATCGGCCTGCAGTTGCCCTTCAGCAGCTGGT
ACGTGGATCGGGGCGGAAACGGCTGTCTGATGGCCCCAGAGGTGTCCACGGCCCGTCCTG
GCCCCAGGGCAGTGATTGACTACAGCAAGGCTGATGCCTGGGCAGTGGGAGCCATCGCCT
ATGAAATCTTCGGGCTTGTCAATCCCTTCTACGGCCAGGGCAAGGCCCACCTTGAAAGCC
GCAGCTACCAAGAGGCTCAGCTACCTGCACTGCCCGAGTCAGTGCCTCCAGACGTGAGAC
AGTTGGTGAGGGCACTGCTCCAGCGAGAGGCCAGCAAGAGACCATCTGCCCGAGTAGCCG
CAAATGTGCTTCATCTAAGCCTCTGGGGTGAACATATTCTAGCCCTGAAGAATCTGAAGT
TAGACAAGATGGTTGGCTGGCTCCTCCAACAATCGGCCGCCACTTTGTTGGCCAACAGGC
TCACAGAGAAGTGTTGTGTGGAAACAAAAATGAAGATGCTCTTTCTGGCTAACCTGGAGT
GTGAAACGCTCTGCCAGGCAGCCCTCCTCCTCTGCTCATGGAGGGCAGCCCTGTGATGTC
CCTGCATGGAGCTGGTGAATTACTAAAAGAACTTGGCATCCTCTGTGTCGTGATGGTCTG
TGAATGGTGAGGGTGGGAGTCAGGAGACAAGACAGCGCAGAGAGGGCTGGTTAGCCGGAA
AAGGCCTCGGGCTTGGCAAATGGAAGAACTTGAGTGAGAGTTCAGTCTGCAGTCCTCTGC
TCACAGACATCTGAAAAGTGAATGGCCAAGCTGGTCTAGTAGATGAGGCTGGACTGAGGA
GGGGTAGGCCTGCATCCACAGAGAGGATCCAGGCCAAGGCACTGGCTGTCAGTGGCAGAG
TTTGGCTGTGACCTTTGCCCCTAACACGAGGAACTCGTTTGAAGGGGGCAGCGTAGCATG
TCTGATTTGCCACCTGGATGAAGGCAGACATCAACATGGGTCAGCACGTTCAGTTACGGG
AGTGGGAAATTACATGAGGCCTGGGCCTCTGCGTTCCCAAGCTGTGCGTTCTGGACCAGC
TACTGAATTATTAATCTCACTTAGCGAAAGTGACGGATGAGCAGTAAGTAAGTAAGTGTG
GGGATTTAAACTTGAGGGTTTCCCTCCTGACTAGCCTCTCTTACAGGAATTGTGAAATAT
TAAATGCAAATTTACAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCC

FIGURE 3

Met Ala

      Val Arg Gln Ala Leu Gly Arg Gly Leu Gln Leu Gly Arg Ala Leu Leu
               5   10   15

      Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly Arg Pro
               20   25   30

      Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp Ala Ala
      35   40   45   50

      Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro Asn Arg
                          55   60   65

      Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg Leu Gln
                  70   75   80

      Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys Gly Arg
                  85   90   95

      Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu Glu Lys
               100   105   110

      Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile Gln Ala
      115   120   125   130

      Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp Thr Arg
                          135   140   145

      Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln Ser Ile
                  150   155   160

      Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro Thr Leu
                  165   170   175

      Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro Gly Arg
               180   185   190

      Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala Pro Gly
      195   200   205   210

      Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile Ser Ala
                          215   220   225

                       FIGURE 3 (c nt'd)

Gly Ser Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu Leu Val
            230   235   240

Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val Thr Tyr
            245   250   255

Arg Lys Ser Lys Arg Gly Pro Lys Gln Leu Ala Pro His Pro Asn Ile
    260   265   270

Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu Pro Gly
275   280   285   290

Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His Pro Glu
            295   300   305

Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn Tyr Pro
            310   315   320

Cys Thr Leu Arg Gln Tyr Leu Cys Val Asn Thr Pro Ser Pro Arg Leu
        325   330   335

Ala Ala Met Met Leu Leu Gln Leu Leu Glu Gly Val Asp His Leu Val
    340   345   350

Gln Gln Gly Ile Ala His Arg Asp Leu Lys Ser Asp Asn Ile Leu Val
355   360   365   370

Glu Leu Asp Pro Asp Gly Cys Pro Trp Leu Val Ile Ala Asp Phe Gly
            375   380   385

Cys Cys Leu Ala Asp Glu Ser Ile Gly Leu Gln Leu Pro Phe Ser Ser
        390   395   400

Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro Glu Val
        405   410   415

Ser Thr Ala Arg Pro Gly Pro Arg Ala Val Ile Asp Tyr Ser Lys Ala
    420   425   430

FIGURE 3 (cont'd)

```
Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly Leu Val

435               440               445               450


Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg Ser Tyr
              455               460               465


Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro Asp Val
              470               475               480


Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys Arg Pro
          485               490               495


Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp Gly Glu
    500               505               510


His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val Gly Trp
515               520               525               530


Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu Thr Glu
              535               540               545


Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala Asn Leu
              550               555               560


Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser Trp Arg
          565               570               575


Ala Ala Leu
```

FIGURE 3 (cont'd)

GTCGACCCACGCGGTC●CCCACGCGTTCCGGAGACATGTC●GTGTTTC
TCTCCCCTCCGCTTTTGAGTCCGTTGAAGACACAATTTCTCTCTGTCGGGT
GCTTAGGAGGAGCTCCATGAACATGTATTGAATTGGACTTAGCTGAACAG
GCTGCTGGTTGGCTGCCCAGAGGGGGCAGGCTGTGTTGCTGGGAGCCTTC
CAGCTCCCTGCAGCAGTCATGGGGCAGGGTTCCCCGAGTCCGTAATCCCC
ATTTCCACCTACTTTCCCTTAGTTATTTGATTCCCTGTCTGTCGTACTCAGC
TTAAGTGGAGCATCCCCTTTCCTGGGAGACACGAAGCAGGAAACACTGGC
AAATATCACAGCAGTGAGTTACGACTTTGATGAGGAATTCTTCAGCCAGA
CGAGCGAGCTGGCCAAGGACTTTATTCGGAAGCTTCTGGTTAAAGAGACC
CGGAAACGGCTCACAATCCAAGAGGCTCTCAGACACCCCTGGATCACGCC
GGTGGACAACCAGCAAGCCATGGTGCGCAGGGAGTCTGTGGTCAATCTGG
AGAACTTCAGGAAGCAGTATGTCCGCAGGCGGTGGAAGCTTTCCTTCAGC
ATCGTGTCCCTGTGCAACCACCTCACCCGCTCGCTGATGAAGAAGGTGCA
CCTGAGGCCGGATGAGGACCTGAGGAACTGTGAGAGTGACACTGAGGAG
GACATCGCCAGGAGGAAAGCCCTCCACCCACGGAGGAGGAGCAGCACCT
CCTAACTGGCCTGACCTGCAGTGGCCGCCAGGGAGGTCTGGGCCCAGCGG
GGCTCCCTTCTGTGCAGACTTTTGGACCCAGCTCAGCACCAGCACCCGGGC
GTCCTGAGCACTTTGCAAGAGAGATGGGCCCAAGGAATTCAGAAGAGCTT
GCAGGCAAGCCAGGAGACCCTGGGAGCTGTGGCTGTCTTCTGTGGAGGAG
GCTCCAGCATTCCCAAAGCTCTTAATTCTCCATAAAATGGGCTTTCCTCTG
TCTGCCATCCTCAGAGTCTGGGGTGGGAGTGTGGACTTAGGAAAACAATA
TAAAGGACATCCTCATCATCACGGGGTGAAGGTCAGACTAAGGCAGCCTT
CTTCACAGGCTGAGGGGGTTCAGAACCAGCCTGGCCAAAAATTACACCAG
AGAGACAGAGTCCTCCCCATTGGGAACAGGGTGATTGAGGAAAGTGAACC
TTGGGTGTGAGGGACCAATCCTGTGACCTCCCAGAACCATGGAAGCCAGG
ACGTCAGGCTGACCAACACCTCAGACCTTCTGAAGCAGCCCATTGCTGGC
CCGCCATGTTGTAATTTTGCTCATTTTTATTAAACTTCTGGTTTACCTGATG
CTTGGCTTCTTTTAGGGCTACCCCCATCTCATTTCCTTTAGCCCGTGTGCCT
GTAACTCTGAGGGGGGGCACCCAGTGGGGTGCTGAGTGGGCAGAATCTCA
GAAGGTCCTCCTGAACCGTCCGCGCAGGCCTGCAGTGGGCCTGCCTCCTC
CTTGCTTCCCTAACAGGAAGGTGTCCAGTTCAAGAGAACCCACCCAGAGA
CTGGGAGTGGTGGCTCACGCCTATAATCCCTGCGCTTTGGCAGTCCGAGG
CAGGGGAATTGCTTGAACTCAGGAGTTGGAGACCAGCCTGGGCAACATGG
CAAAACGCAGTCTGTACAAAAAATACAAAAAATTAGCCAGGTGTAGGGGT
AGGCACCTGGCATCCCAGCTACTCCAGGGGCTGAGGTGACAGCATTGCTT
AAGCCCAGAAGGTCGAGGCTGCAGTGAGCTGAGATCACGCCACTGCACTC
CAGTCTGGGTGACAGAGAGAGACCATATCCAAAAAAAAAAAAAAAAGGG
CGGCCGC

LFDSLSVVLSLSGASPFLGDTKQETLANITAVSYDFDEEFFSQTSELAKDFIRKL
LVKETRKRLTIQEALRHPWITPVDNQQAMVRRESVVNLENFRKQYVRRRWK
LSFSIVSLCNHLTRSLMKKVHLRPDEDLRNCESDTEEDIARRKALHPRRRSSTS

FIGURE 4

```
        T   A   L   A   K   E   L   R   E   L   R   I   E   E   T   N   R   P   M
  G ACG GCA TTA GCC AAA GAA CTA AGA GAA CTC CGG ATT GAA GAA ACA AAC CGC CCA ATG        19
                                                                                        57

      K   K   V   T   D   Y   S   S   S   S   E   E   S   E   S   S   E   E   E   E
  AAG AAG GTG ACT GAT TAC TCC TCC TCC AGT GAG GAG TCA GAA AGT AGC GAG GAA GAG GAG      39
                                                                                       117

      E   D   G   E   S   E   T   H   D   G   T   V   A   V   S   D   I   P   R   L
  GAA GAT GGA GAG AGC GAG ACC CAT GAT GGG ACA GTG GCT GTC AGC GAC ATA CCC AGA CTG      59
                                                                                       177

      I   P   T   G   A   P   G   S   N   E   Q   Y   N   V   G   M   V   G   T   H
  ATA CCA ACA GGA GCT CCA GGC AGC AAC GAG CAG TAC AAT GTG GGA ATG GTG GGG ACG CAT      79
                                                                                       237

      G   L   E   T   S   H   A   D   S   F   S   G   S   I   S   R   E   G   T   L
  GGG CTG GAG ACC TCT CAT GCG GAC AGT TTC AGC GGC AGT ATT TCA AGA GAA GGA ACC TTG      99
                                                                                       297

      M   I   R   E   T   S   G   E   K   K   R   S   G   H   S   D   S   N   G   F
  ATG ATT AGA GAG ACG TCT GGA GAG AAG AAG CGA TCT GGC CAC AGT GAC AGC AAT GGC TTT     119
                                                                                       357

      A   G   H   I   N   L   P   D   L   V   Q   Q   S   H   S   P   A   G   T   P
  GCT GGC CAC ATC AAC CTC CCT GAC CTG GTG CAG CAG AGC CAT TCT CCA GCT GGA ACC CCG     139
                                                                                       417

      T   E   G   L   G   R   V   S   T   H   S   Q   E   M   D   S   G   T   E   Y
  ACT GAG GGA CTG GGG CGC GTC TCA ACC CAT TCC CAG GAG ATG GAC TCT GGG ACT GAA TAT     159
                                                                                       477

      G   M   G   S   S   T   K   A   S   F   T   P   F   V   D   P   R   V   Y   Q
  GGC ATG GGG AGC AGC ACC AAA GCC TCC TTC ACC CCC TTT GTG GAC CCC AGA GTA TAC CAG     179
                                                                                       537

      T   S   P   T   D   E   D   E   E   D   E   E   S   S   A   A   A   L   F   T
  ACG TCT CCC ACT GAT GAA GAT GAA GAG GAT GAG GAA TCA TCA GCC GCA GCT CTG TTT ACT     199
                                                                                       597

      S   E   L   L   R   Q   E   Q   A   K   L   N   E   A   R   K   I   S   V   V
  AGC GAA CTT CTT AGG CAA GAA CAG GCC AAA CTC AAT GAA GCA AGA AAG ATT TCG GTG GTA     219
                                                                                       657

      N   V   N   P   T   N   I   R   P   H   S   D   T   P   E   I   R   K   Y   K
  AAT GTA AAC CCA ACC AAC ATT CGG CCT CAT AGC GAC ACA CCA GAA ATC AGA AAA TAC AAG     239
                                                                                       717

      K   R   F   N   S   E   I   L   C   A   A   L   W   G   V   N   L   L   V   G
  AAA CGA TTC AAC TCA GAA ATA CTT TGT GCA GCT CTG TGG GGT GTA AAC CTT CTG GTG GGG     259
                                                                                       777

      T   E   N   G   L   M   L   L   D   R   S   G   Q   G   K   V   Y   N   L   I
  ACT GAA AAT GGC CTG ATG CTT TTG GAC CGA AGT GGG CAA GGC AAA GTC TAT AAT CTG ATC     279
                                                                                       837

      N   R   R   R   F   Q   Q   M   D   V   L   E   G   L   N   V   L   V   T   I
  AAC CGG AGG CGA TTT CAG CAG ATG GAT GTG CTA GAG GGA CTG AAT GTC CTT GTG ACA ATT     299
                                                                                       897

      S   G   K   K   N   K   L   R   V   Y   Y   L   S   W   L   R   N   R   I   L
  TCA GGA AAG AAG AAT AAG CTA CGA GTT TAC TAT CTT TCA TGG TTA AGA AAC AGA ATA CTA     319
                                                                                       957

      H   N   D   P   E   V   E   K   K   Q   G   W   I   T   V   G   D   L   E   G
  CAT AAT GAC CCA GAA GTA GAA AAG AAA CAA GGC TGG ATC ACT GTT GGG GAC TTG GAA GGC     339
                                                                                      1017

      C   I   H   Y   K   V   V   K   Y   E   R   I   K   F   L   V   I   A   L   K
  TGT ATA CAT TAT AAA GTT GTT AAA TAT GAA AGG ATC AAA TTT TTG GTG ATT GCC TTA AAG     359
                                                                                      1077

      N   A   V   E   I   Y   A   W   A   P   K   P   Y   H   K   F   M   A   F   K
  AAT GCT GTG GAA ATA TAT GCT TGG GCT CCT AAA CCG TAT CAT AAA TTC ATG GCA TTT AAG     379
                                                                                      1137

      S   F   A   D   L   Q   H   K   P   L   L   V   D   L   T   V   E   E   G   Q
  TCT TTT GCA GAT CTC CAG CAC AAG CCT CTG CTA GTT GAT CTC ACG GTA GAA GAA GGT CAA     399
                                                                                      1197

      R   L   K   V   I   P   G   S   H   T   G   F   H   V   I   D   V   D   S   G
                                                                                       419
```

FIGURE 5

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    AGA TTA AAG GTT ATT TTT GGT TCA CAC ACT GGT TTC CAT GTA ATT GAT GTT GAT TCA GGA   1257

     N   S   Y   D   I   Y   I   P   S   H   I   Q   G   N   I   T   P   H   A   I     439
    AAC TCT TAT GAT ATC TAC ATA CCA TCT CAT ATT CAG GGC AAT ATC ACT CCT CAT GCT ATT   1317

     V   I   L   P   K
    GTC ATC TTG CCT AAA                                                                444
                                                                                      1332
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